## REMARKS

Claim 1 has been amended. Thus, claims 1-4 and 6-9 remain pending in the present application. No new matter has been added. Reconsideration and withdrawal of the present rejection in view of the comments presented herein are respectfully requested.

Rejection Under 35 U.S.C. §102(b)

The rejection of Claims 1-4 and 6-9 under 35 U.S.C. §102(b) as allegedly being anticipated by Bruccoleri et al (*Nucl. Acids Res.* **26**:4482-2286, 1998) was maintained.

The Examiner contends that Bruccoleri et al. teach all of the limitations of Claim 1 (generation of overlapping sequence alignments from pathogenic organisms; homolog matching; target sequence alignment for all sequences; alignment of just matching gene product against the corresponding gene product in the target; and exclusion criteria).

Claim 1 as amended recites that extended conserved peptide sequences obtained in step (v) are compared to host organism protein sequences to identify conserved peptide sequences from selected pathogenic organisms which are not present in host proteins. Thus, this claim clearly recites that the target sites are identified at the end of the claimed process, in the absence of any information regarding these target sites at the beginning of the process. In contrast, in the method of Bruccoleri et al., "In order to prepare a concordance of gene products for a given organism, it is necessary to specify the following information. (i) The target genome…" (Emphasis added). Thus, in the method of Bruccoleri et al, the identity of the target genome (i.e., conserved peptide sequences) must be specified at the beginning of the process. In the absence of this information, the process of Bruccoleri et al. cannot be performed. (also see Declaration at paragraph (4d)). Thus, the claims cannot be anticipated by this reference.

In view of the comments presented above, Applicants respectfully request reconsideration and withdrawal of the rejection under 35 U.S.C. §102(b).

The present claims are also not rendered obvious by this reference, since the claimed method has several unexpected, advantageous properties that are not suggested by Bruccoleri et al., nor could they have been predicted based on this reference. Enclosed herewith is a Declaration under 37 C.F.R. § 1.132 by Dr. Debasis Dash, one of the inventors of the present application. In the Declaration at paragraph (4b), Dr. Dash states that the results of the presently

claimed method require half the steps of the method disclosed by Bruccoleri et al. Thus, this method is much more efficient, and would necessarily yield a more accurate result. In addition, as noted in paragraph (4c) of the Declaration, the present method can be practiced with a minimum of 4 amino acids. In contrast, Bruccoleri et al. provide no suggestion that their method can be applied to such short peptide fragments. Lastly, as noted in paragraph (4e) of the Declaration, the nomenclature of the proteins tested in the present application is the same as the international database. Thus, anyone wanting to perform this technique (compared to an unknown protein) can do so with the guidance presented in the present specification. In contrast, the names of the sequences provided in Table 4 of Bruccoleri et al. will not allow the collection of details of the desired sequence from the public domain.

## CONCLUSION

Applicants submit that all claims are in condition for allowance. If any issues remain that could be resolved by telephone, the Examiner is cordially invited to contact the undersigned at the telephone number provided below. Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: 12/3/08

By: _____

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EXHIBIT A

**Brief Biodata**

**Debasis Dash, Ph.D.**
Scientist, G.N. Ramachandran Knowledge Centre for Genome Informatics,
Institute of Genomics and Integrative Biology, CSIR
Mall Road, Delhi - 110 007, India
ddash@igib.res.in

**Research Experience**
**2000-2008**

- Developing the data model and deciphering the relationship between Genotype and Phenotype
- Unraveling the functional significance of unfolded proteins
- Development of Polymorphic Markup Language with the help international collaboration, Indian Genome Variation Database and Genotype to Phenotype Database
- Development of computer based methods for genome analysis for
  (a) identifying peptides useful as drug targets, (b) assigning functions to hypothetical/ orphan proteins, (c) retrieving unique peptides for diagnostics (d) identification of protein coding genes
- Developed & Commercialized Software PLHOST[FA], GenoCluster, HT-SSS and publicly available database CoPS – Comprehensive Peptide Signature Database

**1994-2000**

- Biophysical studies on Ligand – DNA, Protein – DNA interaction and understanding the mechanism DNA condensation
- Understanding the mechanisms of polyglutamine aggregation and its behaviour using biophysical methods

**Patents**

- A computer based method for identifying peptides useful as drug targets
  US, PCT: NF64/2000; Samir K. Brahmachari and Debasis Dash
- A computer based method for predicting protein coding DNA sequences useful as drug targets. US, PCT: NF 421/03; S.K. Brahmachari, D. Dash, J.K Maheshwari and R. Sharma

**Awards and Achievements**

- Awarded Prestigious Fellowship under the scheme of Center for Advance Studies (CAS) from University of Delhi.
- GATE (Graduate Aptitude Test for Engineers) for Chemical Sciences.
- **The CSIR Young Scientis t Award for the year 2004 in Biological sciences** for use of short peptide stretches to relate proteins in different genomes, which have similar function, and also for development of **PLHOST** software and associated databases.

**Important Presentations in International Symposia**

The 5th International Biodata Interoperability Conference, JBIC, Tokyo, Japan September 26 - 29, 2007; The 8th International Meeting on Human Genome Variation and Complex Genome Hong Kong Univ., Hong Kong 14-16 September, 2006; The 4th International Biodata Interoperability Conference, JBIC, Tokyo, Japan Oct 17 - 19, 2006; 2nd Indo-Taiwan Joint workshop on Functional Genomics from 2nd – 5th March, 2006 at National Yang-Ming University, Taipei, Taiwan; International Conference on High Performance Computing (HiPC), Goa, Dec. 18-21, 2005; 3rd International Biodata Interoperability Conference, Yokohama, Japan, Sep. 5–8, 2005; Second Indo French Bioinformatics Meeting, St Dennis, La Reunion, Dec. 9-13, 2004. Sino-India Workshop on Genome Informatics, HANGZOU and BEIJING, CHINA, 27 Oct. – 02 Nov. 2004; 5th International conference on Learning to Manage in WTO Borderless Regime, Jan 7th, 2004; University of Manchester, Mar 15, 2003.

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EXHIBIT A

**Debasis Dash, Ph.D.**
Scientist, G.N.R Knowledge Centre
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**Selected Publications**

1. Intrinsic disorder in yeast transcriptional regulatory network
   Singh GP, and **Dash Debasis**.
   **Proteins: Structure, Function & Bioinformatics**, 68(3):602-5 (2007)

2. Dynamic alpha-helices: conformations that do not conform
   Sandhu KS, and **Dash Debasis**.
   **Proteins: Structure, Function & Bioinformatics,** 68(1):109-22 (2007)

3. Role of intrinsic disorder in transient interactions of hub proteins.
   Singh GP, Ganapathi M, and **Dash Debasis**
   **Proteins: Structure, Function & Bioinformatics**, 66(4):761-5 (2007)

4. Conformational flexibility may explain the multiple cellular roles of PEST motifs
   Sandhu KS and **Dash Debasis**
   **Proteins: Structure, Function & Bioinformatics**, 63:727–732 (2006)

5. Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes.
   Singh GP,Ganapathi M, Sandhu KS and **Dash Debasis**
   **Proteins: Structure, Function & Bioinformatics**, 62:309-315 (2006)

6. The Indian Genome Variation database (IGVdb): a project overview.
   **The Indian Genome Variation Consortium**
   **Hum Genet** (2005) 118: 1–11.

7. Conformational Analysis of Invariant Peptide Sequences in Bacterial Genomes
   Tulika Prakash, C. Ramakrishnan, **Debasis Dash** and Samir K. Brahmachari
   **J Mol Biol.** 2005 Feb 4;345(5):937-55.

8. Comparative analysis of protein unfoldedness in human housekeeping and non - housekeeping proteins.
   Neeraj Pandey, Mythily Ganapathi, Kaushal Kumar, Dipayan Dasgupta, Sushanta Das Sutar, **Debasis Dash**
   **Bioinformatics**, 2004 Jun; PMID: 15238363

9. CoPS: Comprehensive Peptide Signature Database.
   Tulika Prakash, Mamta Khandelwal, Dipayan Dasgupta, Debasis Dash, Samir K. Brahmachari
   **Bioinformatics**, 2004 May; PMID: 15166019

10. Recognition and analysis of protein coding genes in Severe Acute Respiratory Syndrome associated Coronavirus.
    Sharma Ramakant, Maheshwari Jitendra Kumar, Prakash Tulika, **Dash Debasis**, Brahmachari Samir K.
    **Bioinformatics**, 2004 Feb; PMID: 14764577

11. Role of histidine interruption in mitigating the pathological effects of long polyglutamine stretches in SCA1: A molecular approach.
    Somdutta Sen , **Debasis Dash**, Santosh Pasha, Samir K. Brahmachari
    **Protein Science**, 2003 May;12(5):953-962.

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Name: Debasis Dash
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**Scholastic Details**

| Degree | Subject | Class | Year | University | Additional Particulars |
|---|---|---|---|---|---|
| B.Sc | Chemistry (Hons.), Physics, Mathematics | 1st | 1992 | Utkal University | Hons. With Distinction |
| M.Sc | Physical Chem(Spl.) | 1st | 1994 | Delhi University | Second in the Specialisation |
| Ph.D | Biophysical Chemistry | | 1998 | Delhi University | ***Studies on the effect of methylphosphonate substitution and 2',5'-linkages on the stability of alternating C/G oligodeoxynucleotides and the condensation of DNA by basic oligopeptides*** |

Work experience

| S.No | Period | Place of Employment | Designation |
|---|---|---|---|
| 1. | Dec 2004 – till date | Institute of Genomics and Integrative Biology | Scientist E-I |
| 2. | Dec 2001 – Dec 2004 | Institute of Genomics and Integrative Biology | Scientist C |
| 1. | May 2000-Dec 2001 | Institute of Genomics and Integrative Biology(Formerly Known as Center for Biochemical technology) | Scientist Fellow (Quick Hire Scheme) |
| 2. | Apr 1998- May 2000 | Institute of Genomics and Integrative Biology(Formerly Known as CBT) | Research Associate |